

INFLUENCE OF BACTERIAL COMMUNITIES ON PARTICLE AGGREGATION

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LONG-TERM GOALS

The long term goals of this research are to determine the identity, roles, and influence of bacteria associated with marine aggregation processes. These data will ultimately be used to develop accurate predictive models of coagulation in nature, which take into account relevant physical, chemical and biological parameters.

OBJECTIVES

Our main objective is to determine the microbial composition, colonization, and patterns of succession occurring on marine aggregates. We are also interested in microbial processes occurring on aggregates, such as bacterial production and enzymatic hydrolysis. When these details are in hand, we will determine how microbial populations alter the aggregation potential of transparent exopolymer particles (TEP) and organic aggregates.

APPROACH

Our approach consists of collecting and analyzing both natural and laboratory-made particles. Nucleic acid sequencing and hybridization techniques, in conjunction with more standard methods, are used to identify the specific types of bacteria associated with naturally-occurring particles. By generating "artificial" aggregates under controlled conditions in the laboratory, we are assessing microbial variability and succession, as well as the processes mediated by particle-associated bacteria on time scales relevant to particle formation, flocculation, and disaggregation. This detailed information on *in situ* bacterial colonization and succession will allow us to assess the influence of bacteria on particle formation and disaggregation. Bacterial processes will be assessed using standard methods including measurement of bacterial production rate and exopolymer hydrolysis rates.

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WORK COMPLETED

In year four of the project we analyzed the data from our 1200 liter mesocosm experiments. Specifically, we studied the colonization of detrital aggregates and population dynamics of both aggregate (AGG) and free-living (FL) communities. This included the variation of the phylogenetic composition of the bacterial assemblage with other biological and biochemical factors- including bacterial abundance, exo-enzyme activity, and leucine incorporation. Additionally, we tested the hypotheses that Cytophaga-like bacteria (CLB), which are known to produce exo-cellular enzymes, are important in the early stages of marine snow diagenesis and that hydrolytic activity on macroaggregates can be correlated with the CLB population. A manuscript on the phylogenetic composition of microbial populations on mesopelagic aggregates was submitted to Deep Sea Research (Fowler et al., submitted). Paul Fowler, the graduate student supported by this grant, will complete his Ph D in early 1998.

RESULTS

The mesocosm results so far indicate highly dynamic microbial communities, as both the free-living and the aggregate attached bacteria show rapid shifts in abundance over time. Members of the CLB population were shown to be important components of attached microbial populations especially in the early stages of marine snow diagenesis. As the particles aged their abundance/activity, based on DNA hybridization studies, declined from 25 to 12% of the bacterial rRNA signal. Our results show differential specific enzyme hydrolysis between free-living and attached microbial assemblages. The attached microbial assemblages had greater total and cell specific enzyme activities. The peak enzyme activity appeared near the end of marine snow diagenesis, while the maximum cytophaga rRNA occurred earlier in particle formation. Thus, particle associated CLB rRNA maxima did not correlate directly with particle associated exoenzyme activity. There are several explanations for these results. One possibility is that exoenzymes are produced by CLBs under nutrient stress, after phytoplankton bloom demise. Therefore, CLB rRNA maxima do not correlate directly with particle associated exoenzyme activity maxima. Another possibility is that bacterial populations that were not quantified by hybridization studies are responsible for the observed exoenzyme activity.

IMPACTS

Aggregated particulate matter has been shown to be important to sedimentation, nutrient cycling and optical properties of the water column. Potentially, bacteria play a role in aggregation and solubilization of the particles, thus affecting the concentrations, size distributions and formation of aggregates. Our work in identification of members of the microbial community and their activities will allow us to more fully understand the role of bacteria in determining size distributions and aggregation/disaggregation processes in the ocean.

TRANSITIONS

None applicable

RELATED PROJECTS

This research was strongly tied to the now completed SIGMA ARI (Significant Interactions Governing Marine Aggregation). We continue to interact with the PI's from this ARI, especially George Jackson of Texas A&M University and Farooq Azam of Scripps Institution of Oceanography.

References

Fowler, P. D., K.Y. Wu, H. Rath, and E.F.Delong. Comparison of aggregate-attached and free-living marine bacterial assemblages from the surface to mesopelagic depths in the Santa Barbara Channel. Deep-Sea Research. Submitted